# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/836,540
Source: 1Fw/6
Date Processed by STIC: 1/3/06

# *ENTERED*

IFW16

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 3 <110> APPLICANT: Seed, Brian
 4        Aruffo, Alejandro
 5        Camerini, David
 7 <120> TITLE OF INVENTION: CD27 Coding Sequence
 9 <130> FILE REFERENCE: 11-88L
11 <140> CURRENT APPLICATION NUMBER: US 09/836,544D
12 <141> CURRENT FILING DATE: 2001-04-17
14 <150> PRIOR APPLICATION NUMBER: US 07/983,647
15 <151> PRIOR FILING DATE: 1992-12-01
17 <150> PRIOR APPLICATION NUMBER: US 07/553,759
18 <151> PRIOR FILING DATE: 1990-07-13
20 <150> PRIOR APPLICATION NUMBER: US 07/498,809
21 <151> PRIOR FILING DATE: 1990-03-23
23 <150> PRIOR APPLICATION NUMBER: US 07/379,076
24 <151> PRIOR FILING DATE: 1989-07-13
26 <150> PRIOR APPLICATION NUMBER: US 07/160,416
27 <151> PRIOR FILING DATE: 1988-02-25
29 <160> NUMBER OF SEQ ID NOS: 41
31 <170> SOFTWARE: PatentIn version 3.3
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2932
35 <212> TYPE: DNA
36 <213> ORGANISM: artificial
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Nucleotide sequence of piH3 vector
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44 gatcaagagc taccaactct ttttccgaag gaactggctt cagcagagcg cagataccaa    120
46 atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcaccgc    180
48 ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc gataagtcgt    240
50 gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tcgggctgaa    300
52 cggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc    360
54 tacagcgtga gctatgagaa agcgccacgc ttcccgaagg agaaaggcg gacaggtatc     420
56 cggtaagcgg cagggtcgga acaggagagc gcacgaggga gcttccaggg ggaaacgcct    480
58 ggtatcttta tagtcctgtc gggtttcgcc acctctgact tgagcgtcga ttttgtgat     540
60 gctcgtcagg ggggcggagc ctatggaaaa acgccagcaa cgccgaatta ccgcggtgtt    600
62 tctcaacgta cactttaca gcggcgcgtc atttgatatg atgcgcccg cttcccgata     660
64 agggagcagg ccagtaaaag cattacccgt ggtggggttc ccgagcggcc aaagggagca    720
66 gactctaaat ctgccgtcat cgacttcgaa ggttcgaatc cttcccccac caccatcact    780
68 ttcaaaagtc cgaaagaatc tgctccctgc ttgtgtgttg gaggtcgctg agtagtgcgc    840
70 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcatga agaatctgct    900
72 tagggttagg cgttttgcgc tgcttcgcga tgtacgggcc agatatacgc gttgacattg    960
74 attattgact agttattaat agtaatcaat tacggggtca ttagttcata gcccatatat   1020
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RAW SEQUENCE LISTING          DATE: 01/03/2006
PATENT APPLICATION:   US/09/836,544D      TIME: 14:39:37

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Output Set: N:\CRF4\01032006\I836544D.raw

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 80 ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac atcaagtgta   1200
 82 tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg cctggcatta   1260
 84 tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg tattagtcat   1320
 86 cgctattacc atggtgatgc ggttttggca gtacatcaat gggcgtggat agcggtttga   1380
 88 ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt tttggcacca   1440
 90 aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg   1500
 92 aattcctggg cgggactggg gagtggcgag ccctcagatg ctgcatataa gcagctgctt   1560
 94 tttgcctgta ctgggtctct ctggttagac cagatctgag cctgggagct ctctggctaa   1620
 96 ctagagaacc cactgcttaa gcctcaataa agcttctaga gatccctcga cctcgaggga   1680
 98 tcttccatac ctaccagttc tgcgcctgca ggtcgcggcc gcgactctag aggatctttg   1740
100 tgaaggaacc ttacttctgt ggtgtgacat aattggacaa actacctaca gagatttaaa   1800
102 gctctaaggt aaatataaaa tttttaagtg tataatgtgt taaactactg attctaattg   1860
104 tttgtgtatt ttagattcca acctatggaa ctgatgaatg ggagcagtgg tggaatgcct   1920
106 ttaatgagga aaacctgttt tgctcagaag aaatgccatc tagtgatgat gaggctactg   1980
108 ctgactctca acattctact cctccaaaaa agaagagaaa ggtagaagac cccaaggact   2040
110 ttccttcaga attgctaagt tttttgagtc atgctgtgtt tagtaataga actcttgctt   2100
112 gctttgctat ttacaccaca aaggaaaaag ctgcactgct atacaagaaa attatggaaa   2160
114 aatattctgt aacctttata agtaggcata acagttataa tcataacata ctgttttttc   2220
116 ttactccaca caggcataga gtgtctgcta ttaataacta tgctcaaaaa ttgtgtacct   2280
118 ttagcttttt aatttgtaaa ggggttaata aggaatattt gatgtatagt gccttgacta   2340
120 gagatcataa tcagccatac cacatttgta gaggttttac ttgctttaaa aaacctccca   2400
122 cacctccccc tgaacctgaa acataaaatg aatgcaattg ttgttgttaa cttgtttatt   2460
124 gcagcttata atggttacaa ataaagcaat agcatcacaa atttcacaaa taaagcattt   2520
126 ttttcactgc attctagttg tggtttgtcc aaactcatca atgtatctta tcatgtctgg   2580
128 atcctgtgga atgtgtgtca gttagggtgt ggaaagtccc caggctcccc agcaggcaga   2640
130 agtatgcaaa gcatgcatct caattagtca gcaaccaggt gtggaaagtc cccaggctcc   2700
132 ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccat agtcccgccc   2760
134 ctaactccgc ccatcccgcc cctaactccg cccagttccg cccattctcc gccccatggc   2820
136 tgactaattt tttttattta tgcagaggcc gaggccgcct cggcctctga gctattccag   2880
138 aagtagtgag gaggcttttt tggaggccta ggcttttgca aaaagctaat tc           2932
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142 <211> LENGTH: 1504
143 <212> TYPE: DNA
144 <213> ORGANISM: Homo sapiens
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148 <221> NAME/KEY: CDS
149 <222> LOCATION: (7)..(1059)
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154         1               5                  10
156 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc        96
157 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
158 15                  20                  25                  30
160 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct       144
161 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
162                 35                  40                  45
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164 agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act    192
165 Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
166          50              55                  60
168 tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc    240
169 Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe
170          65                  70                  75
172 aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att    288
173 Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile
174          80                  85                  90
176 aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat    336
177 Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
178 95                  100                 105                 110
180 gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att    384
181 Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
182                  115                 120                 125
184 caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca    432
185 Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
186                  130                 135                 140
188 acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg    480
189 Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu
190          145                 150                 155
192 tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac    528
193 Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His
194          160                 165                 170
196 aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac    576
197 Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn
198 175                 180                 185                 190
200 aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa    624.
201 Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys
202                  195                 200                 205
204 ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc    672
205 Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu
206          210                 215                 220
208 ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa    720
209 Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys
210          225                 230                 235
212 aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac    768
213 Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His
214          240                 245                 250
216 aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct    816
217 Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala
218 255                 260                 265                 270
220 tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct    864
221 Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro
222                  275                 280                 285
224 ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac    912
225 Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His
226                  290                 295                 300
228 cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca    960
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229 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr
230         305                 310                 315
232 caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag      1008
233 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
234         320                 325                 330
236 cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct      1056
237 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser
238 335                 340              .  345                 350
240 aat taaaaaagat agaaactgtc tttttcaata aaaagcactg tggatttctg           1109
241 Asn
244 ccctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca    1169
246 cctcctgagg ctgtgggcca cagccacctc tgcatcttcg aactcagcca tgtggtcaac    1229
248 atctggagtt tttggtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa   .1289
250 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct    1349
252 ctcaggtcat gtgtagatgc gataaatcaa gtgattggtg tgcctgggtc tcactacaag    1409
254 cagcctatct gcttaagaga ctctggagtt tcttatgtgc cctggtggac acttgcccac    1469
256 catcctgtga gtaaaagtga aataaaagct ttgac                               1504
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260 <211> LENGTH: 351
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
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271             20                  25                  30
274 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
275         35                  40          .       45
278 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
279     50                  55                  60
282 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu .
283 65                  70                  75                  80
286 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
287             85                  90          .       95
290 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
291             100                 105                 110
294 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
295             115                 120                 125
298 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
299     130                 135                 140
302 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
303 145                 150                 155                 160
306 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
307             165                 170                 175
310 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
311             180                 185                 190
314 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
315             195                 200                 205
318 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
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322 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
323 225                     230                     235                     240
326 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
327                     245                     250                     255
330 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
331                     260                     265                     270
334 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
335             275                     280                     285
338 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
339         290                     295                     300
342 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
343 305                     310                     315                     320
346 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
347                     325                     330                     335
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351                 340                     345                     350
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355 <211> LENGTH: 874
356 <212> TYPE: DNA
357 <213> ORGANISM: Homo sapiens
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361 <221> NAME/KEY: CDS
362 <222> LOCATION: (13)..(723)
364 <400> SEQUENCE: 4
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367              1               5                       10
369 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt        99
370 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
371     15                  20                  25
373 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta       147
374 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
375 30                  35                  40                  45
377 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat       195
378 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
379                 50                  55                  60
381 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt       243
382 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
383             65                  70                  75
385 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac       291
386 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
387         80                  85                  90
389 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat       339
390 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
391     95                  100                 105
393 att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca       387
394 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
395 110                 115                 120                 125
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        RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 01/03/2006
        PATENT APPLICATION:  US/09/836,544D       TIME: 14:39:38

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        Output Set: N:\CRF4\01032006\I836544D.raw
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**Please Note:**
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:38; Xaa Pos. 1,4

**Invalid <213> Response:**
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,6,37,38

**VERIFICATION SUMMARY**                    DATE: 01/03/2006
PATENT APPLICATION:   **US/09/836,544D**         TIME: 14:39:38

Input Set  : **A:\11-88L.ST25.txt**
Output Set: **N:\CRF4\01032006\I836544D.raw**

L:3794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0